

#9

OIPE

RAW SEQUENCE LISTING DATE: 07/05/2001  
PATENT APPLICATION: US/09/881,853 TIME: 11:11:57

Input Set : A:\PTO.txt  
Output Set: N:\CRF3\07032001\I881853.raw

ANT: YIN, AMY  
IA, SHERI  
Y, WAYNE  
DAVID  
OF INVENTION: HUMAN HEMTOPOIETIC STEM AND PROGENITOR CELL ANTIGEN AND

REFERENCE: AMCE-012/02US  
T APPLICATION NUMBER: US/09/881,853  
T FILING DATE: 2001-06-13  
APPLICATION NUMBER: 08/842,382  
FILING DATE: 1997-04-23  
APPLICATION NUMBER: 08/639,891  
FILING DATE: 1996-04-26  
OF SEQ ID NOS: 2  
RE: PatentIn version 3.0  
NO: 1  
: 3804  
DNA  
SM: Homo sapiens  
E:  
KEY: CDS  
DN: (38)..(2632)  
CE: 1

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1 5  
ctg ctg ggg ctg tgc ggg aac tcc ttt tca gga ggg cag 103  
Leu Leu Gly Leu Cys Gly Asn Ser Phe Ser Gly Gly Gln  
10 15 20  
aca gat gct cct aag gct tgg aat tat gaa ttg cct gca 151  
Thr Asp Ala Pro Lys Ala Trp Asn Tyr Glu Leu Pro Ala  
30 35  
gag acc caa gac tcc cat aaa gct gga ccc att ggc att 199  
Glu Thr Gln Asp Ser His Lys Ala Gly Pro Ile Gly Ile  
45 50  
cta gtg cat atc ttt ctc tat gtg gta cag ccg cgt gat 247  
Leu Val His Ile Phe Leu Tyr Val Val Gln Pro Arg Asp  
60 65 70  
tat act ttg aga aaa ttc tta cag aag gca tat gaa tcc 295  
Asp Thr Leu Arg Lys Phe Leu Gln Lys Ala Tyr Glu Ser  
75 80 85  
at gac aag cca gaa act gta atc tta ggt cta aag att 343  
Tyr Asp Lys Pro Glu Thr Val Ile Leu Gly Leu Lys Ile  
90 95 100  
aa gca ggg att att cta tgc tgt gtc ctg ggg ctg ctg 391  
Glu Ala Gly Ile Ile Leu Cys Cys Val Leu Gly Leu Leu  
110 115

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65	ttt att att ctg atg cct ctg gtg ggg tat ttc ttt tgt atg tgt cgt	439
66	Phe Ile Ile Leu Met Pro Leu Val Gly Tyr Phe Phe Cys Met Cys Arg	
67	120 125 130	
69	tgc tgt aac aaa tgt ggt gga gaa atg cac cag cga cag aag gaa aat	487
70	Cys Cys Asn Lys Cys Gly Gly Glu Met His Gln Arg Gln Lys Glu Asn	
71	135 140 145 150	
73	ggg ccc ttc ctg agg aaa tgc ttt gca atc tcc ctg ttg gtg att tgt	535
74	Gly Pro Phe Leu Arg Lys Cys Phe Ala Ile Ser Leu Leu Val Ile Cys	
75	155 160 165	
77	ata ata ata agc att ggc atc ttc tat ggt ttt gtg gca aat cac cag	583
78	Ile Ile Ile Ser Ile Gly Ile Phe Tyr Gly Phe Val Ala Asn His Gln	
79	170 175 180	
81	gta aga acc cgg atc aaa agg agt cgg aaa ctg gca gat agc aat ttc	631
82	Val Arg Thr Arg Ile Lys Arg Ser Arg Lys Leu Ala Asp Ser Asn Phe	
83	185 190 195	
85	aag gac ttg cga act ctc ttg aat gaa act cca gag caa atc aaa tat	679
86	Lys Asp Leu Arg Thr Leu Leu Asn Glu Thr Pro Glu Gln Ile Lys Tyr	
87	200 205 210	
89	ata ttg gcc cag tac aac act acc aag gac aag gcg ttc aca gat ctg	727
90	Ile Leu Ala Gln Tyr Asn Thr Thr Lys Asp Lys Ala Phe Thr Asp Leu	
91	215 220 225 230	
93	aac agt atc aat tca gtg cta gga ggc gga att ctt gac cga ctg aga	775
94	Asn Ser Ile Asn Ser Val Leu Gly Gly Ile Leu Asp Arg Leu Arg	
95	235 240 245	
97	ccc aac atc atc cct gtt ctt gat gag att aag tcc atg gca aca gcg	823
98	Pro Asn Ile Ile Pro Val Leu Asp Glu Ile Lys Ser Met Ala Thr Ala	
99	250 255 260	
101	atc aag gag acc aaa gag gcg ttg gag aac atg aac agc acc ttg aag	871
102	Ile Lys Glu Thr Lys Glu Ala Leu Glu Asn Met Asn Ser Thr Leu Lys	
103	265 270 275	
105	agc ttg cac caa caa agt aca cag ctt agc agc agt ctg acc agc gtg	919
106	Ser Leu His Gln Gln Ser Thr Gln Leu Ser Ser Leu Thr Ser Val	
107	280 285 290	
109	aaa act agc ctg cgg tca tct ctc aat gac cct ctg tgc ttg gtg cat	967
110	Lys Thr Ser Leu Arg Ser Ser Leu Asn Asp Pro Leu Cys Leu Val His	
111	295 300 305 310	
113	cca tca agt gaa acc tgc aac agc atc aga ttg tct cta agc cag ctg	1015
114	Pro Ser Ser Glu Thr Cys Asn Ser Ile Arg Leu Ser Leu Ser Gln Leu	
115	315 320 325	
117	aat agc aac cct gaa ctg agg cag ctt cca ccc gtg gat gca gaa ctt	1063
118	Asn Ser Asn Pro Glu Leu Arg Gln Leu Pro Pro Val Asp Ala Glu Leu	
119	330 335 340	
121	gac aac gtt aat aac gtt ctt agg aca gat ttg gat ggc ctg gtc caa	1111
122	Asp Asn Val Asn Asn Val Leu Arg Thr Asp Leu Asp Gly Leu Val Gln	
123	345 350 355	
125	cag ggc tat caa tcc ctt aat gat ata cct gac aga gta caa cgc caa	1159
126	Gln Gly Tyr Gln Ser Leu Asn Asp Ile Pro Asp Arg Val Gln Arg Gln	
127	360 365 370	
129	acc acg act gtc gta gca ggt atc aaa agg gtc ttg aat tcc att ggt	1207

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130	Thr	Thr	Thr	Val	Val	Ala	Gly	Ile	Lys	Arg	Val	Leu	Asn	Ser	Ile	Gly	
131	375				380				385								390
133	tca	gat	atc	gac	aat	gta	act	cag	cgt	ctt	cct	att	cag	gat	ata	ctc	1255
134	Ser	Asp	Ile	Asp	Asn	Val	Thr	Gln	Arg	Leu	Pro	Ile	Gln	Asp	Ile	Leu	
135						395				400						405	
137	tca	gca	ttc	tct	gtt	tat	gtt	aat	aac	act	gaa	agt	tac	atc	cac	aga	1303
138	Ser	Ala	Phe	Ser	Val	Tyr	Val	Asn	Asn	Thr	Glu	Ser	Tyr	Ile	His	Arg	
139						410				415						420	
141	aat	tta	cct	aca	ttg	gaa	gag	tat	gat	tca	tac	tgg	tgg	ctg	ggt	ggc	1351
142	Asn	Leu	Pro	Thr	Leu	Glu	Tyr	Asp	Ser	Tyr	Trp	Trp	Leu	Gly	Gly		
143						425				430						435	
145	ctg	gtc	atc	tgc	tct	ctg	acc	ctc	atc	gtg	att	ttt	tac	tac	ctg		1399
146	Leu	Val	Ile	Cys	Ser	Leu	Leu	Thr	Leu	Ile	Val	Ile	Phe	Tyr	Tyr	Leu	
147						440				445						450	
149	ggc	tta	ctg	tgt	ggc	gtg	tgc	ggc	tat	gac	agg	cat	gcc	acc	ccg	acc	1447
150	Gly	Leu	Leu	Cys	Gly	Val	Cys	Gly	Tyr	Asp	Arg	His	Ala	Thr	Pro	Thr	
151						455				460						470	
153	acc	cga	ggc	tgt	gtc	tcc	aac	acc	gga	ggc	gtc	ttc	ctc	atg	gtt	gga	1495
154	Thr	Arg	Gly	Cys	Val	Ser	Asn	Thr	Gly	Gly	Val	Phe	Leu	Met	Val	Gly	
155						475				480						485	
157	gtt	gga	tta	agt	ttc	ctc	ttt	tgc	tgg	ata	ttg	atg	atc	att	gtg	gtt	1543
158	Val	Gly	Leu	Ser	Phe	Leu	Phe	Cys	Trp	Ile	Leu	Met	Ile	Ile	Val	Val	
159						490				495						500	
161	ctt	acc	ttt	gtc	ttt	ggt	gca	aat	gtg	gaa	aaa	ctg	atc	tgt	gaa	cct	1591
162	Leu	Thr	Phe	Val	Phe	Gly	Ala	Asn	Val	Glu	Lys	Leu	Ile	Cys	Glu	Pro	
163						505				510						515	
165	tac	acg	agc	aag	gaa	tta	tcc	cgg	gtt	ttg	gat	aca	ccc	tac	tta	cta	1639
166	Tyr	Thr	Ser	Lys	Glu	Leu	Phe	Arg	Val	Leu	Asp	Thr	Pro	Tyr	Leu	Leu	
167						520				525						530	
169	aat	gaa	gac	tgg	gaa	tac	tat	ctc	tct	ggg	aag	cta	ttt	aat	aaa	tca	1687
170	Asn	Glu	Asp	Trp	Glu	Tyr	Tyr	Leu	Ser	Gly	Lys	Leu	Phe	Asn	Lys	Ser	
171						535				540						550	
173	aaa	atg	aag	ctc	act	ttt	gaa	caa	gtt	tac	agt	gac	tgc	aaa	aaa	aat	1735
174	Lys	Met	Lys	Leu	Thr	Phe	Glu	Gln	Val	Tyr	Ser	Asp	Cys	Lys	Lys	Asn	
175						555				560						565	
177	aga	ggc	act	tac	ggc	act	ctt	cac	ctg	cag	aac	agc	ttc	aat	atc	agt	1783
178	Arg	Gly	Thr	Tyr	Gly	Thr	Leu	His	Leu	Gln	Asn	Ser	Phe	Asn	Ile	Ser	
179						570				575						580	
181	gaa	cat	ctc	aac	att	aat	gag	cat	act	gga	agc	ata	agc	agt	gaa	ttg	1831
182	Glu	His	Leu	Asn	Ile	Asn	Glu	His	Thr	Gly	Ser	Ile	Ser	Ser	Glu	Leu	
183						585				590						595	
185	gaa	agt	ctg	aag	gta	aat	ctt	aat	atc	ttt	ctg	ttg	ggt	gca	gca	gga	1879
186	Glu	Ser	Leu	Lys	Val	Asn	Leu	Asn	Ile	Phe	Leu	Leu	Gly	Ala	Ala	Gly	
187						600				605						610	
189	aga	aaa	aac	ctt	cag	gat	ttt	gct	gct	tgt	gga	ata	gac	aga	atg	aat	1927
190	Arg	Lys	Asn	Leu	Gln	Asp	Phe	Ala	Ala	Cys	Gly	Ile	Asp	Arg	Met	Asn	
191						615				620						630	
193	tat	gac	agc	tac	ttg	gct	cag	act	ggt	aaa	tcc	ccc	gca	gga	gtg	aat	1975
194	Tyr	Asp	Ser	Tyr	Leu	Ala	Gln	Thr	Gly	Lys	Ser	Pro	Ala	Gly	Val	Asn	

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195	635	640	645	
197	ctt tta tca ttt gca tat gat cta gaa gca aaa gca aac agt ttg ccc			2023
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201	cca gga aat ttg agg aac tcc ctg aaa aga gat gca caa act att aaa			2071
202	Pro Gly Asn Leu Arg Asn Ser Leu Lys Arg Asp Ala Gln Thr Ile Lys			
203	665	670	675	
205	aca att cac cag caa cga gtc ctt cct ata gaa caa tca ctg agc act			2119
206	Thr Ile His Gln Gln Arg Val Leu Pro Ile Glu Gln Ser Leu Ser Thr			
207	680	685	690	
209	cta tac caa agc gtc aag ata ctt caa cgc aca ggg aat gga ttg ttg			2167
210	Leu Tyr Gln Ser Val Lys Ile Leu Gln Arg Thr Gly Asn Gly Leu Leu			
211	695	700	705	710
213	gag aga gta act agg att cta gct tct ctg gat ttt gct cag aac ttc			2215
214	Glu Arg Val Thr Arg Ile Leu Ala Ser Leu Asp Phe Ala Gln Asn Phe			
215	715	720	725	
217	atc aca aac aat act tcc tct gtt att att gag gaa act aag aag tat			2263
218	Ile Thr Asn Asn Thr Ser Ser Val Ile Ile Glu Glu Thr Lys Lys Tyr			
219	730	735	740	
221	ggg aga aca ata ata gga tat ttt gaa cat tat ctg cag tgg atc gag			2311
222	Gly Arg Thr Ile Ile Gly Tyr Phe Glu His Tyr Leu Gln Trp Ile Glu			
223	745	750	755	
225	tcc tct atc agt gag aaa gtg gca tcg tgc aaa cct gtg gcc acc gct			2359
226	Phe Ser Ile Ser Glu Lys Val Ala Ser Cys Lys Pro Val Ala Thr Ala			
227	760	765	770	
229	cta gat act gct gtt gat gtc ttt ctg tgt agc tac att atc gac ccc			2407
230	Leu Asp Thr Ala Val Asp Val Phe Leu Cys Ser Tyr Ile Ile Asp Pro			
231	775	780	785	790
233	ttg aat ttg ttt tgg ttt ggc ata gga aaa gct act gta ttt tta ctt			2455
234	Leu Asn Leu Phe Trp Phe Gly Ile Gly Lys Ala Thr Val Phe Leu Leu			
235	795	800	805	
237	ccg gct cta att ttt gcg gta aaa ctg gct aag tac tat cgt cga atg			2503
238	Pro Ala Leu Ile Phe Ala Val Lys Leu Ala Lys Tyr Tyr Arg Arg Met			
239	810	815	820	
241	gat tcg gag gac gtg tac gat gat gtt gaa act ata ccc atg aaa aat			2551
242	Asp Ser Glu Asp Val Tyr Asp Asp Val Glu Thr Ile Pro Met Lys Asn			
243	825	830	835	
245	atg gaa aat ggt aat aat ggt tat cat aaa gat cat gta tat ggt att			2599
246	Met Glu Asn Gly Asn Asn Gly Tyr His Lys Asp His Val Tyr Gly Ile			
247	840	845	850	
249	cac aat cct gtt atg aca agc cca tca caa cat tgatagctga tgttgaaact			2652
250	His Asn Pro Val Met Thr Ser Pro Ser Gln His			
251	855	860	865	
253	gcttgaggcat caggatactc aaagtggaaa ggatcacaga tttttggtag tttctgggtc			2712
255	tacaaggact ttccaaatcc aggagcaacg ccagtggcaa cgtatgtact caggcgccc			2772
257	ccaggcaac ggcaccattg gtctctgggt agtgcttaa gaatgaacac aatcacgtta			2832
259	tagtccatgg tccatcacta ttcaaggatg actccctccc ttccctgtcta tttttgttt			2892
261	ttactttttt acactgagtt tctattnaga cactacaaca tatggggtgt ttgttccccat			2952
263	tggatgcatt tctatcaaaa ctctatcaaa tgtgatggct agattcta ac atattgccat			3012

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265	gtgtggagt	tgctgaacac	acaccagtt	acaggaaaga	tgcatttgt	gtacagtaaa	3072
267	cggtgtatat	acctttgtt	accacagat	ttttaaaca	aatgagtatt	ataggactt	3132
269	cttctaaatg	agctaaataa	gtcaccattg	acttcttgg	gctgttggaa	ataatccatt	3192
271	ttcaactaaaa	gtgtgtgaaa	cctacacatc	atttttcacg	cagagattt	catotattat	3252
273	actttatcaa	agattggcca	tgttccactt	ggaaatggca	tgcaaaagcc	atcatagaga	3312
275	aacctcgta	actccatctg	acaaattcaa	aagagagaga	gagatctga	gagagaaatg	3372
277	ctgttcgttc	aaaagtggag	ttgttttaac	agatccat	tacggtgtac	agtttaacag	3432
279	agttttctgt	tgcatttagga	taaacattaa	ttggagtgca	gctaacatga	gtatcatcag	3492
281	actagtatca	agtgttctaa	aatgaaatat	gagaagatcc	tgtcacaatt	cttagatctg	3552
283	gtgtccagca	tggatgaaac	ctttggat	ggccctaaa	tttgcatgaa	agcacaaggt	3612
285	aaatattcat	ttgcttcagg	agtttcatgt	tggatctgtc	attatcaaaa	gtgtcagca	3672
287	atgaagaact	ggtcggacaa	aatttaacgt	tgtatgtatg	gaattccaga	tgttaggcatt	3732
289	ccccccaggt	cttttcatgt	gcagattgca	gttctgattc	atttgaataa	aaaggaactt	3792
291	ggaaaaaaaaa	aa					3804
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295	<211>	LENGTH:	865				
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297	<213>	ORGANISM:	Homo sapiens				
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305	Ser Phe Ser Gly Gly Gln Pro Ser Ser	Thr	Asp Ala Pro Lys Ala Trp				
306	20	25	30				
309	Asn Tyr Glu Leu Pro Ala Thr Asn Tyr Glu Thr Gln Asp Ser His Lys						
310	35	40	45				
313	Ala Gly Pro Ile Gly Ile Leu Phe Glu Leu Val His Ile Phe Leu Tyr						
314	50	55	60				
317	Val Val Gln Pro Arg Asp Phe Pro Glu Asp Thr Leu Arg Lys Phe Leu						
318	65	70	75	80			
321	Gln Lys Ala Tyr Glu Ser Lys Ile Asp Tyr Asp Lys Pro Glu Thr Val						
322	85	90	95				
325	Ile Leu Gly Leu Lys Ile Val Tyr Tyr Glu Ala Gly Ile Ile Leu Cys						
326	100	105	110				
329	Cys Val Leu Gly Leu Leu Phe Ile Ile Leu Met Pro Leu Val Gly Tyr						
330	115	120	125				
333	Phe Phe Cys Met Cys Arg Cys Cys Asn Lys Cys Gly Gly Glu Met His						
334	130	135	140				
337	Gln Arg Gln Lys Glu Asn Gly Pro Phe Leu Arg Lys Cys Phe Ala Ile						
338	145	150	155	160			
341	Ser Leu Leu Val Ile Cys Ile Ile Ile Ser Ile Gly Ile Phe Tyr Gly						
342	165	170	175				
345	Phe Val Ala Asn His Gln Val Arg Thr Arg Ile Lys Arg Ser Arg Lys						
346	180	185	190				
349	Leu Ala Asp Ser Asn Phe Lys Asp Leu Arg Thr Leu Leu Asn Glu Thr						
350	195	200	205				
353	Pro Glu Gln Ile Lys Tyr Ile Leu Ala Gln Tyr Asn Thr Thr Lys Asp						
354	210	215	220				
357	Lys Ala Phe Thr Asp Leu Asn Ser Ile Asn Ser Val Leu Gly Gly						
358	225	230	235	240			

**VERIFICATION SUMMARY**

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date